

Page 1

Alignments									
RESULT 1									
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ered. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Gencore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:47:35 : Search time 7.42225 Seconds
 (Without alignments) Million cell updates/sec
 1607.447

Title: US-10-724-274-1
 Perfect score: 657
 Sequence: 1 QVQLKESGPGLVAPSQSLSI.....TTGTDALDYCQGTSTVSS 124

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR80*;

1: Pirl1*;

2: Pir2*;

3: Pir3*;

4: Pir4*;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510	77.6	144	2 S11244	Ig gamma-2a chain
2	503	76.6	122	2 S22809	Ig heavy chain v r
3	500.5	76.2	144	1 GMMS14	Ig heavy chain pre
4	499	76.0	117	2 S38563	Ig heavy chain v r
5	492	74.9	141	2 S52446	Ig heavy chain v r
6	490	74.6	120	2 P1.0087	Ig heavy chain v r
7	489	74.4	122	2 A43049	Ig heavy chain v r
8	488.5	74.4	140	2 S55028	Ig heavy chain v r
9	484.5	73.7	114	2 S11106	Ig heavy chain v r
10	478.5	72.8	112	2 S11100	Ig heavy chain v r
11	478.5	72.4	111	2 S26324.	Ig heavy chain v r
12	473	72.0	139	2 A32456	Ig heavy chain pre
13	472.5	71.9	231	2 PC155	Ig gamma-2b chain
14	470	71.5	118	2 S32186	Ig heavy chain (an
15	469.5	71.5	112	2 S11108	Ig heavy chain v r
16	468.5	71.5	116	2 S11102	Ig heavy chain v r
17	469.5	71.5	140	2 S14238	Ig gamma-1 chain p
18	469	71.4	116	2 S42484	Ig heavy chain v r
19	468.5	71.3	110	2 S26323	Ig heavy chain v r
20	467.5	71.2	113	2 S11101	Ig heavy chain v r
21	466	70.9	101	2 S03466	Ig heavy chain v r
22	466	70.9	135	2 S31913	Ig gamma-2A chain
23	465.5	70.9	118	2 PQ046	Ig heavy chain v r
24	463.5	70.5	114	2 S11099	Ig heavy chain v r
25	463.5	70.5	127	2 B31807	Ig heavy chain v r
26	459.5	69.8	115	2 S11103	Ig heavy chain v r
27	457.5	69.6	106	2 S26322	Ig heavy chain v r
28	455.5	69.2	106	2 S14489	Ig heavy chain v r
29	452.5	68.9	121	2 D30560	Ig heavy chain v r

RESULT 1

S11244

Ig gamma-2a chain precursor - mouse (fragment)

C;Species: *Mus musculus* (house mouse)

C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C;Accession: S11244

R;Wellman, A.A.; Meares, C.P.

Nucleic Acids Res. 18, 5281, 1990

A;Title: Sequences of the Lyt-1 antibody heavy and light chain variable regions.

A;Reference number: S11244; MUID:90381832; PMID:2119497

A;Molecule type: mRNA

A;Accession: S11244

A;Residues: 1-144 <WEL>

A;Cross-references: UNIPARC:UPI0000176C81; EMBL:X53483

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 77.6%: Score 510; DB 2; Length 144;

Best Local Similarity 81.5%; Pred. No. 1.6e-38; Mismatches 6; Indels 6; Gaps 2;

Matches 101; Conservative 81.5%;

Qy

1 QVQLKESGPGLVAPSQSLITCTISGFLSLDYGHWRQPPGKGLEWLVIVWSDGSSSTYN 60

Db

20 QVQLKESGPGLVAPSQSLITCTISGFLSLDYGHWRQPPGKGLEWLVIVWSDGSSSTYN 79

Qy

61 SALKERMTIRDNKNSQVFLIMNSQTDSSAMYCARHGTYYGMTTGQGTSV 120

Db

80 SALKERUSISKDNSKNSQVFLIMNSQTDIAYKQASH--YGSTL--AFASWGHSTLV 133

Qy

121 TWS 124

Db

134 TWSA 137

Qy

RESULT 2

S20809

Ig heavy chain V region (hybridoma C8) - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C;Accession: S20809

R;Hoogenboom, H.; Dubois, P.; Raus, J.; Volckaert, G.

A;Submitted to the EMBL Data Library, September 1990

A;Description: Nucleotide sequences of the variable region cDNAs encoding a murine ant

A;Accession: S20809

A;Molecule type: mRNA

A;Residues: 1-122 <HCO>

A;Cross-references: UNIPARC:UPI0000115E8E; EMBL:X54692; NID:950249; PIDN:CAA38508.1; E

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

ALIGMENTS

protein - protein search, using SW model						
Copyright (c) 1993 - 2006 Biocceleration Ltd.						
on:		June 6, 2006, 04:37:25 : Search time 57.3611 Seconds			(without alignments)	
		1999.647 Million cell updates/sec				
title:	US-10-724-274-1	perfect score:	657	sequence:	1 QVQLKESGPGLVAPSOSLSI.....TTTGDAALDYWGQGSTSVTVSS	124
scoring table:	BLOSUM62	gapop:	10.0	gapext:	0.5	
archeved:	2849598 seqs, 925015592 residues	total number of hits satisfying chosen parameters:	2849598			
database:	UniProt 7.2: 1: uniprot_sprot: 2: uniprot_trembl: *	Maximum DB seq length:	0	Minimum DB seq length:	2000000000	
post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
result No.	Score	Query Length	DB ID		Description	
1	500.5	76.2	144	1	HV43_MOUSE	P01819 mus muscu
2	499	76.0	484	2	Q51472_MOUSE	Q5u472 mus muscu
3	483	73.5	121	2	Q93X92_MOUSE	Q91x92 mus muscu
4	481	73.2	121	2	Q93X94_MOUSE	Q99194 mus muscu
5	470	71.5	591	2	Q51019_RAT	Q51019 rattus no
6	456.5	67.7	469	2	Q50839_RAT	Q5m339 rattus no
7	444.5	67.7	477	2	Q51001_RAT	Q51011 rattus no
8	435.5	66.3	458	2	Q50842_RAT	Q5m842 rattus no
9	435	66.2	115	1	HV44_MOUSE	P01820 mus muscu
10	406	61.8	1	1	HV45_MOUSE	P01821 mus muscu
11	379	57.7	485	2	Q561M5_MOUSE	Q561M5 mus muscu
12	376.5	57.3	487	2	Q586B5_MOUSE	Q58653 rattus no
13	373	56.8	135	1	HV02_XENIA	P20557 xenopus 1
14	373	56.8	483	2	Q51413_MOUSE	Q5u413 mus muscu
15	367	55.9	560	2	Q417801_XENLA	Q4v01 xenopus 1
16	367	55.9	573	2	Q80738_HUMAN	Q8vn38 homo sapi
17	364.5	55.5	485	2	Q58554_MOUSE	Q58554 mus muscu
18	363	55.3	617	2	Q559B3_RAT	Q55935 rattus no
19	357.5	55.4	476	2	Q6GMK1_HUMAN	Q6gmx1 homo sapi
20	354.5	54.0	119	2	Q90173_HUMAN	Q9u173 homo sapi
21	352.5	53.7	121	1	HV30_HUMAN	P01771 homo sapi
22	351	53.4	477	2	Q6GMK7_HUMAN	Q6gmx7 homo sapi
23	350.5	53.3	240	2	Q562C9_HUMAN	Q652c9 homo sapi
24	350	53.3	118	2	Q811U5_MOUSE	Q811u5 rattus no
25	350	53.3	478	2	Q5FV03_RAT	Q5fv03 rattus no
26	349.5	53.2	472	2	Q6N089_HUMAN	Q6n089 homo sapi
27	349	53.1	465	2	Q6GMK6_HUMAN	Q6gmx6 homo sapi
28	349	53.1	469	2	Q562F4_HUMAN	Q562f4 homo sapi
29	346	52.7	126	1	HV3K_HUMAN	P01772 homo sapi
30	345.5	52.6	136	1	Q011_XENLA	Q011 xenopus 1
31	345.5	52.6	615	2	Q565F6_RAT	Q565f6 rattus no

32	52.4	493	2	QBNCL6_HUMAN	Q8n16	homo sapien
33	52.4	122	1	HV3G_HUMAN	P01768	homo sapien
34	52.4	467	2	Q4YBH1_RAT	Q4ybh1	rattus norvegicus
35	52.4	482	2	Q5V1R6_RAT	Q5v1r6	rattus norvegicus
36	52.4	496	2	Q96KX8_HUMAN	Q96kx8	homo sapien
37	52.2	136	2	Q6LBQ5_MOUSE	Q6lbq5	mus musculus
38	52.1	116	2	Q9WJ93_HUMAN	Q9wj93	homo sapien
39	52.5	121	2	Q9D9J6_HUMAN	Q9d9j6	homo sapien
40	52.5	485	2	Q6PDB8_MOUSE	Q6pdb8	mus musculus
41	52.1	136	1	HV16_MOUSE	P01783	mus musculus
42	52.1	613	2	Q8W4K1_HUMAN	Q8w4k1	homo sapien
43	51.8	576	2	Q6P418_HUMAN	Q6p418	homo sapien
44	51.8	620	2	Q96SY0_HUMAN	Q96sy0	homo sapien
45	51.7	121	2	Q9U7J1_HUMAN	Q9u7j1	homo sapien

ATTACHMENT 5

RESULT 1		RESULT 2	
HV43	MOUSE	HV43	MOUSE
ID	HV43_3	ID	STANDARD
AC	PO1819;	AC	PRT;
DT	21-JUL-1986,	DT	144 AA.
	Integrated into UniProtKB/Swiss-Prot.		
	21-JUL-1986, sequence version 1.		
DT	07-MAR-2006, entry version 44.		
DB	Ig heavy chain V region MOPC 141 precursor		
OS	Mus musculus (Mouse)		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Gliridae; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.		
OC	Uncharacterized protein 1.000000		

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description					
result	No.	Score	Query	Match	Length	DB	ID
1	500.5	76.2	144	1	HV43	MOUSE	P01819
2	499	76.0	484	2	Q5M472	MOUSE	P01820
3	483	73.5	482	2	Q91392	MOUSE	Q91x92
4	481	73.2	121	2	Q99n44	MOUSE	Q99ng4
5	470	71.5	591	2	Q51019	RAT	Q51019
6	455.5	69.9	469	2	Q5M839	RAT	Q5m839
7	444.5	67.7	477	2	Q51011	RAT	Q51011
8	435.5	66.3	458	2	Q5M842	RAT	Q5m842
9	435	66.1	115	1	HV44	MOUSE	P01820
10	406	61.8	116	1	HV45	MOUSE	P01821
11	379	57.7	485	2	Q56155	MOUSE	Q56155
12	376.5	57.7	487	2	Q58853	MOUSE	Q58853
13	373	56.8	135	1	HV20	XENLA	P20957
14	373	56.8	483	2	Q5U13	MOUSE	Q5u413
15	367	55.9	560	2	Q4VB01	XENLA	Q4r7801
16	367	55.9	573	2	Q8W338	HUMAN	Q8w338
17	364.5	55.5	495	2	Q58854	MOUSE	Q58854
18	363	55.3	617	2	Q56193	RAT	Q56193
19	357.5	54.4	476	2	Q6GK01	HUMAN	Q6GK01
20	354.5	54.0	119	2	Q9UJ73	HUMAN	Q9UJ73
21	352.5	53.7	121	1	HV31	HUMAN	P01772
22	351	53.4	477	2	Q6GK07	HUMAN	Q6GK07
23	350.5	53.3	240	2	Q6S2C9	HUMAN	Q6S2C9
24	350	53.3	118	2	Q811U5	MOUSE	Q811U5
25	350	53.3	478	2	Q5FV03	RAT	Q5FV03
26	349.5	53.2	472	2	Q6N085	HUMAN	Q6N085
27	349	53.1	465	2	Q6GMX6	HUMAN	Q6GMX6
28	349	53.1	469	2	Q569F4	HUMAN	Q569F4
29	346	53.1	126	1	HV3K	HUMAN	P01772
30	345.5	52.6	615	2	Q569F6	RAT	Q569F6
31	345.5	52.6	615	2	Xenopus	XENLA	P02056

Query Match Score 500.5; DB 1; Length 144;
 Best-Local Similarity 76.2%; Pred. No. 1; 3e-42;
 Matches 98; Conservative 7; Mismatches 19; Indels 1; Gaps 1

QY 1 QVQKESGGLVIAVPSQSLSTCTISGFSLTDYGVWVROPPGKGLEMLVIVWSGDSSTYN 6

DR Complete annotation from a
 RL Nature 286:676-683 (1980).
 CC -1- MISCELLANEOUS: The sequence shown is translated from a
 CC differentiatied gene isolated from a myeloma that secretes IgG2b.
 CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC
 EMBL: J00491; AAA38121.1; -; Genomic_DNA.
 DR PIR: A02094; G2NS14.
 DR HSSP: P01820; 1G7J.
 DR P01813; 20-144.
 DR Ensembl: ENSMUSG000000063075; Mus musculus.
 DR IPR003599; Ig.
 DR IPR007110; Ig-like.
 DR IPR003596; Ig-V.
 DR IPR013106; V-set.
 DR PF07666; V-set; 1.
 DR SMART: SM00409; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PSS0835; Ig_LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; signal.
 FT SIGNAL 1 19
 FT CHAIN 20 144 Ig heavy chain V region MOPC 141.
 FT /PRD=PRO_0000015229.
 FT DOMAIN 20 130 Ig-like.
 FT NON_TER 144 144
 SEQ SEQUENCE 144 AA; 15759 MW; 8B47A7CB3706D30A CRC64;

Géncore version 5.1.9
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OM protein - protein search, using SW model

Run on: June 6, 2006, 04:59:30 ; Search time 15.0722 seconds

(without alignments)
830.460 Million cell updates/sec

Title: US-10-724-274-16

Perfect score: 752
Sequence: 1 MAVGLLPLCLVTFPSCTVLSQ.....TTGGDALDYGQGTSTVSS 143

Scoring table: BLOSUM62

Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:
1: /EMC_Celerra_SIDS3/prodata/2/iaa/5_COMB.pep:
2: /EMC_Celerra_SIDS3/prodata/2/iaa/6_COMB.pep:
3: /EMC_Celerra_SIDS3/prodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SIDS3/prodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/prodata/2/iaa/RB_COMB.pep:
7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574	76.3	135	2 US-10-351-748-31	Sequence 31, App1
2	574.5	76.1	142	3 US-09-722-103-4	Sequence 4, App1
3	571	75.9	137	1 US-08-621-751A-4	Sequence 4, App1
4	570.5	75.9	152	1 US-08-752-844-4	Sequence 4, App1
5	570.5	75.9	152	1 US-08-591-196-4	Sequence 4, App1
6	570.5	75.9	152	2 US-09-192-838B-4	Sequence 4, App1
7	570.5	75.9	152	2 US-09-293-533-4	Sequence 4, App1
8	570.5	75.9	152	2 US-09-324-191-4	Sequence 4, App1
9	570.5	75.9	263	1 US-08-752-844-66	Sequence 66, App1
10	570.5	75.9	263	2 US-09-293-533-66	Sequence 66, App1
11	552.5	73.5	478	2 US-09-722-916-2	Sequence 2, App1
12	542.5	72.1	138	1 US-07-634-278-33	Sequence 33, App1
13	542.5	72.1	138	1 US-08-477-128-33	Sequence 33, App1
14	542.5	72.1	138	1 US-08-474-040-33	Sequence 33, App1
15	542.5	72.1	138	1 US-08-487-200-33	Sequence 33, App1
16	542.5	72.1	138	1 US-08-484-337-33	Sequence 33, App1
17	542.5	72.1	138	3 US-09-718-998-33	Sequence 33, App1
18	541.5	72.0	140	2 US-08-943-136-4	Sequence 4, App1
19	541.5	72.0	140	2 US-08-973-518-4	Sequence 4, App1
20	522.5	69.5	142	3 US-09-772-103-10	Sequence 10, App1
21	517.5	68.8	119	1 US-08-752-844-16	Sequence 16, App1
22	517.5	68.8	119	1 US-08-591-196-16	Sequence 16, App1
23	517.5	68.8	119	2 US-09-293-333-16	Sequence 16, App1
24	517	68.8	137	1 US-08-621-751A-8	Sequence 8, App1
25	502	66.8	120	1 US-08-552-558-38	Sequence 8, App1
26	500.5	66.6	119	2 US-09-726-219A-187	Sequence 187, App1

RESULT 1
US-10-351-748-31

/ Sequence 31, Application US/10351748

/ Patent No. 6982321

/ GENERAL INFORMATION: IN OR RELATING TO ALTERED

/ APPLICANT: Winter, Gregory Paul

/ TITLE OF INVENTION: IMPROVEMENT IN

/ FILE REFERENCE: 7806-011-993 (CRM 107814-999010)

/ CURRENT APPLICATION NUMBER: US/10/351,748

/ PRIOR FILING DATE: 2003-01-24

/ PRIOR APPLICATION NUMBER: 08/452,462

/ PRIOR FILING DATE: 1995-05-26

/ PRIOR APPLICATION NUMBER: 07/942,146

/ PRIOR FILING DATE: 1992-09-08

/ PRIOR APPLICATION NUMBER: 07/624,515

/ PRIOR FILING DATE: 1990-12-07

/ PRIOR APPLICATION NUMBER: 07/189,814

/ PRIOR FILING DATE: 1988-05-03

/ NUMBER OF SEQ ID NOS: 59

/ SOFTWARE: PasteSEQ for Windows Version 4.0

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

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/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

/ SEQ ID NO 31

/ LENGTH: 135

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE: Amino acid sequence of the variable domain gene of

/ OTHER INFORMATION: antibody D1.3 (Fig 7)

/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

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/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

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/ FEATURE: Amino acid sequence of the variable domain gene of

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/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

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/ LENGTH: 135

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/ US-10-351-748-31

/ Query Match 76.3%; Score 574; DB 2; Length 135;

/ Best Local Similarity 76.9%; Pred. No. 1.2e-48; Mismatches 11; Gaps 8; Gaps 1;

/ Matches 110; Conservative 111; Mismatches 14; Gaps 8; Gaps 1;

<p

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

On protein - protein search, using sw model

Run on: June 6, 2006, 04:37:25 ; Search time 66.1503 seconds
 (without alignments 1999.647 Million cell updates/sec)

Title: US-10-724-274-16
 Perfect score: 752
 Sequence: 1 MAVLGILLCLVTFPSCVLQS.....TTTGDALDYGQGTSTVTS 143

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2:
 1: uniprot_sprot:
 2: uniprot_trembl:
 * 1: uniprot_sprot:
 * 2: uniprot_trembl:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	594	Q5u172	Q5u172	79.0	MOUSE	Q5u172	mus musculus
2	580.5	HV43	HV43	77.2	MOUSE	P01819	mus musculus
3	588	Q91X92	Q91X92	72.5	MOUSE	Q5i019	rattus norvegicus
4	548	Q51019	Q51019	72.9	RAT	Q5m839	rattus norvegicus
5	537.5	Q51019	Q51019	71.5	RAT	Q5i111	rattus norvegicus
6	529.1	Q51019	Q51019	70.4	RAT	Q5m842	rattus norvegicus
7	521.5	Q51019	Q51019	69.3	RAT	P01820	mus musculus
8	519	Q51019	Q51019	69.0	RAT	P01821	mus musculus
9	497	HV44	HV44	66.1	MOUSE	Q99594	mus musculus
10	481	Q99594	Q99594	64.0	MOUSE	Q56165	mus musculus
11	400	Q56165	Q56165	53.2	MOUSE	Q5u113	mus musculus
12	399.5	Q5u113	Q5u113	53.1	XENOMA	P20575	xenopus laevis
13	398.5	P01821	P01821	53.0	XENOMA	Q58853	mus musculus
14	397.5	Q58853	Q58853	52.9	MOUSE	Q4V801	xenopus laevis
15	377	Q4V801	Q4V801	52.6	MOUSE	Q6gmx1	homo sapiens
16	385.5	Q6gmx1	Q6gmx1	51.3	MOUSE	Q58854	mus musculus
17	385.5	Q58854	Q58854	51.3	MOUSE	Q56393	rattus norvegicus
18	384	Q56393	Q56393	51.1	MOUSE	Q6gmx7	homo sapiens
19	379	Q6gmx7	Q6gmx7	50.4	MOUSE	Q6gmx6	homo sapiens
20	377	Q6gmx6	Q6gmx6	50.1	HUMAN	Q56396	rattus norvegicus
21	377	Q56396	Q56396	50.1	RAT	P20536	xenopus laevis
22	373.5	P20536	P20536	49.7	XENOMA	Q961x8	homo sapiens
23	372	Q961x8	Q961x8	49.5	XENOMA	Q6lbq5	mus musculus
24	371.5	Q6lbq5	Q6lbq5	49.4	XENOMA	Q8w338	homo sapiens
25	371.5	Q8w338	Q8w338	49.4	HUMAN	Q56911	homo sapiens
26	368.5	Q56911	Q56911	49.0	HUMAN	Q5p418	homo sapiens
27	368	Q5p418	Q5p418	48.9	HUMAN	Q96ey0	homo sapiens
28	368	Q96ey0	Q96ey0	48.9	HUMAN	P01812	mus musculus
29	366	P01812	P01812	48.7	HUMAN	Q5v16	rattus norvegicus
30	365	Q5v16	Q5v16	48.5	RAT	Q7z379	homo sapiens
31	361	Q7z379	Q7z379	48.0	HUMAN		

ALIGNMENTS

32	360.5	47.9	Q3bbr4	rattus norvegicus
33	356	47.3	Q5fv03	rattus norvegicus
34	356	47.3	Q9nh22	mus musculus
35	355	47.2	Q95973	homo sapiens
36	355	47.2	Q4vh1	rattus norvegicus
37	355	47.2	Q569b8	rattus norvegicus
38	354.5	47.1	Q9u173	homo sapiens
39	354	47.1	Q6n089	homo sapiens
40	352.5	46.9	P01771	homo sapiens
41	352	46.8	Q5674	homo sapiens
42	350.5	46.6	Q65ic9	homo sapiens
43	350	46.5	Q811u5	mus musculus
44	347.5	46.2	Q6pd88	mus musculus
45	347	46.1	HV16	MOUSE

32	360.5	47.9	Q3bbr4	RAT
33	356	47.3	Q5fv03	RAT
34	356	47.3	Q9nh22	MOUSE
35	355	47.2	Q95973	HUMAN
36	355	47.2	Q4vh1	RAT
37	355	47.2	Q569b8	RAT
38	354.5	47.1	Q9u173	HUMAN
39	354	47.1	Q6n089	homo sapiens
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36	355	47.2	Q4vh1	RAT
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38	354.5	47.1	Q9u173	HUMAN
39	354	47.1	Q6n089	homo sapiens
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33	356	47.3	Q5fv03	RAT
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35	355	47.2	Q95973	HUMAN
36	355	47.2	Q4vh1	RAT
37	355	47.2	Q569b8	RAT
38	354.5	47.1	Q9u173	HUMAN
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45	347	46.1	HV16	MOUSE

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33	356	47.3	Q5fv03	RAT
34	356	47.3	Q9nh22	MOUSE
35	355	47.2	Q95973	HUMAN
36	355	47.2	Q4vh1	RAT
37	355	47.2	Q569b8	RAT
38	354.5	47.1	Q9u173	HUMAN
39	354	47.1	Q6n089	homo sapiens
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32	360.5	47.9	Q3bbr4	RAT
33	356	47.3	Q5fv03	RAT
34	356	47.3	Q9nh22	MOUSE
35	355	47.2	Q95973	HUMAN
36	355	47.2	Q4vh1	RAT
37	355	47.2	Q569b8	RAT
38	354.5	47.1	Q9u173	HUMAN
39	354	47.1	Q6n089	homo sapiens
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44	347.5	46.2	Q6pd88	mus musculus
45	347	46.1	HV16	MOUSE

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33	356	47.3	Q5fv03	RAT
34	356	47.3	Q9nh22	MOUSE
35	355	47.2	Q95973	HUMAN
36	355	47.2	Q4vh1	RAT
37	355	47.2	Q569b8	RAT
38	354.5	47.1	Q9u173	HUMAN
39	354	47.1	Q6n089	homo sapiens
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41	352	46.8	Q5674	homo sapiens
42	350.5	46.6	Q65ic9	homo sapiens
43	350	46.5	Q811u5	MOUSE
44	347.5	46.2	Q6pd88	mus musculus
45	347	46.1	HV16	MOUSE

32	360.5	47.9	Q3bbr4	RAT
33	356	47.3	Q5fv03	RAT

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OM protein - protein search, using sw model.

Run on: June 6, 2006, 04:37:11 : search time 51.8517 seconds
(without alignments) 1199.218 Million cell updates/sec

Title: US-10-724-274-20
Perfect score: 722
Sequence: 1 MAVGLLCLVTFPSCVLSQ.....HGTYYGMMTTGDAIPLYWGQG 136

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0\$
Listing first 45 summaries

Database : A_Genesecp_8:*

- 1: genesecp1980s:*
- 2: genesecp1990s:*
- 3: genesecp2000s:*
- 4: genesecp2001s:*
- 5: genesecp2002s:*
- 6: genesecp2003s:*
- 7: genesecp2003bs:*
- 8: genesecp2004s:*
- 9: genesecp2005s:*
- 10: genesecp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	722	100.0	136	9	AEB51157		Aeb51157 Chimeric
2	722	100.0	143	8	ADQ31879		Adq1879 Antibody
3	722	100.0	143	8	ADQ31905		Adq1905 Murine an
4	722	100.0	143	8	ADQ31875		Adq1875 Antibody
5	722	100.0	143	8	ADT77638		Adt77638 Antibody
6	722	100.0	143	8	ADT77634		Adt77634 Antibody
7	722	100.0	143	9	AEB51153		Aeb51153 Chimeric
8	722	100.0	143	9	AEB51180		Aeb51180 Chimeric
9	722	100.0	143	9	AED49294		Aed49294 Anti-alpha
10	722	100.0	143	9	AED49290		Aed49290 Anti-alpha
11	627	86.8	124	8	ADT77619		Adt77619 VH P
12	627	86.8	124	9	AEB51138		Aeb51138 Mouse ant
13	627	86.8	232	8	ADQ31887		Adq31887 Antibody
14	627	86.8	232	8	ADT77646		Adt77646 Antibody
15	627	86.8	232	9	ABB51165		Abb51165 Chimeric
16	627	86.8	451	8	ADQ31684		Adq31684 Antibody
17	627	86.8	451	8	ADT51712		Adt51712 M200 anti
18	627	86.8	451	8	ADT51711		Adt51711 M200 anti
19	627	86.8	451	8	ADT51709		Adt51709 M200 anti
20	627	86.8	451	8	ADT51713		Adt51713 M200 anti
21	627	86.8	451	8	ADT51710		Adt51710 M200 anti
22	627	86.8	451	8	ADT77643		Adt77643 Antibody
23	627	86.8	451	9	AEB51162		Aeb51162 Chimeric

Alignments

RESULT 1

ID AEB51157 standard; protein; 136 AA.

XX AEB51157;

XX DT 06-OCT-2005 (first entry)

XX DE

XX XX

XX Integrin alpha-5/beta-1; chimeric antibody; antibody engineering;

KW angiogenesis disorder; ocular disease; ophthalmological; antidiabetic;

KW antiangiogenic; cardiovascular disease; macular degeneration;

KW diabetic retinopathy; retinal neovascularization; vascularization;

XX KW

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

XX XX

XX PN US2005163769-A1.

XX PD 28-JUL-2005.

XX PP 23-APR-2004; 2004US-00830956.

XX PR 26-NOV-2002; 2002US-0429743P.

PR 30-SEP-2003; 2003US-0508149P.

PR 26-NOV-2003; 2003US-00724274.

XX XX

XX PA (RAMAKRISHNAN V.

PA (POWERS D.

PA (JOHNSON D. B.

PA (JEFFRY U.

XX XX

XX PI Ramakrishnan V.

PI Powers D.

PI Johnson D. B.

PI Jeffry U.

XX XX

XX DR WPI-2005-521374/53.

DR N-PPDB; ABB51156.

PT New chimeric anti-alpha-5beta-1 integrin antibody-5/beta-1, useful for treating angiogenesis-associated ocular disease, ocular disease, or a growth factor-associated ocular disease.

PT The invention relates to a novel chimeric anti-alpha-5/beta-1 integrin

1 protein - protein search, using SW model

Copyright (c) 1993 - 2006 Biocceleration Ltd.

on: June 6, 2006, 04:59:30 ; Search time 14.3344 Seconds
(without alignments)

830.460 Million cell updates/sec

Article: US-10-724-274-20

Score: 722

Sequence: 1 MAVLGLLCLVTPSSCVLSQ.....HGTYKGMTTGDAIDRWGQG 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scanned: 650591 seqs, 87530628 residues

Actual number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries

Issued Patents A1:*

- 1: /EMC_Celerra_SIDS3/prodata/2/iaa/5_COMB_pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/iaa/6_COMB_pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/iaa/7_COMB_pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/iaa/8_COMB_pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/iaa/9_COMB_pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/iaa/10_COMB_pep:*
- 7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfiles1/pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	550	76.2	135	2	US-10-351-748-31
2	548.5	76.0	142	3	US-09-772-103-4
3	54.7	75.8	137	1	US-08-621-751A-4
4	540.5	74.9	152	1	US-08-752-844-4
5	540.5	74.9	152	1	US-08-591-196-4
6	540.5	74.9	152	2	US-09-192-838B-4
7	540.5	74.9	152	2	US-09-293-533-4
8	540.5	74.9	152	2	US-09-324-191-4
9	540.5	74.9	263	1	US-08-752-844-46
10	540.5	74.9	263	2	US-09-293-533-66
11	522.5	72.2	478	2	US-09-770-916-2
12	521.5	72.2	138	1	US-07-634-278-33
13	521.5	72.2	138	1	US-08-477-728-33
14	521.5	72.2	138	1	US-08-474-040-33
15	521.5	72.2	138	1	US-08-487-200-33
16	521.5	72.2	138	2	US-08-484-537-33
17	521.5	72.2	138	3	US-09-718-998-33
18	515.5	71.4	140	2	US-08-943-136-4
19	515.5	71.4	140	2	US-08-973-518-4
20	498.5	69.0	142	3	US-09-772-103-10
21	493	68.3	137	1	US-08-621-751A-8
22	487.5	67.5	119	1	US-08-752-844-16
23	487.5	67.5	119	2	US-09-293-533-16
24	487.5	67.5	119	2	US-09-293-533-16
25	473.5	65.6	272	2	US-09-726-219A-183
26	473.5	65.6	272	1	US-08-652-558-38
27	473.5	65.6	120	2	US-08-881-037-67
28	472	65.4	121	2	US-09-726-219A-218
29	471	65.2	113	2	US-09-726-219A-218
30	468.5	64.9	113	2	US-09-196-522-218
31	468.5	64.9	113	2	US-09-196-522-218
32	468.5	64.9	113	2	US-08-122-546-12
33	466.5	64.6	107	1	US-08-764-938-12
34	466.5	64.6	107	1	US-09-131-052-12
35	466.5	64.6	107	1	US-09-131-053A-12
36	466.5	64.6	107	2	US-10-056-052A-12
37	466.5	64.6	121	2	US-10-056-052A-12
38	466	64.5	112	2	US-09-189-129-3
39	466	64.5	112	2	US-09-824-286-3
40	466	64.5	116	2	US-09-232-290-36
41	466	64.5	239	1	US-08-860-174A-2
42	464.5	64.3	222	1	US-08-190-199A-67
43	464.5	64.3	235	1	US-08-190-199A-61
44	462	64.0	116	2	US-10-194-975-100
45	455	63.0	107	1	US-07-942-245-14

ALIGNMENTS

RESULT 1

US-10-351-748-31

; Sequence 31, Application US/10351748

; Patent No. 6982321

; GENERAL INFORMATION:

; APPLICANT: WING, Gregory Paul

; TITLE OF INVENTION: IMPROVEMENT IN OR RELATING TO ALTERED

; TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 7806-01-99 (CAM 107814-999010)

; CURRENT APPLICATION NUMBER: US/10/351,748

; CURRENT FILING DATE: 2003-01-24

; PRIOR APPLICATION NUMBER: 08/452,462

; PRIOR FILING DATE: 1995-05-26

; PRIOR APPLICATION NUMBER: 07/942,146

; PRIOR FILING DATE: 1992-09-08

; PRIOR APPLICATION NUMBER: 07/624,515

; PRIOR FILING DATE: 1990-12-07

; PRIOR APPLICATION NUMBER: 07/189,814

; NUMBER OF SEQ ID NOS: 59

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO: 31

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence of the variable domain gene of

; OTHER INFORMATION: antibody D1.3 (Fig 7)

US-10-351-748-31

Query Match 76.2%; Score 550; DB 2; Length 135;

Best Local Similarity 77.2%; Pred. No. 1.5e-46;

Matches 105; Conservative 9; Mismatches 14; Indels 8; Gaps 1

Qy 1 MAVGLILCLVTPPSCLVSYOVLKSGPGLVAPSQSLITCTISGFSLTDXGVHWQRP 60

Db 1 MAVLALFLCFLVTPPSCLVSYOVLKSGPGLVAPSQSLITCTISGFSLTDXGVHWQRP 60

Qy 61 GKGLEWLWVWSDGSSYNSALKSMTIRKDNKSKSYQFLMNSLQTDSSAMTCARHGTY 120

Db 61 GKGLEWLWVWGDGTNDYNSALKSRLSISKDSQVFLKNSLHTDARYCARBDY 120

Qy 61 GKGLEWLWVWGDGTNDYNSALKSRLSISKDSQVFLKNSLHTDARYCARBDY 120

Qy 121 YGMMTGTGDAIDWQG 136

Db 121 -----RLDYWQGQ 128

RESULT 2

US-09-772-103-4

GenCore version 5.1.9
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OM protein - protein search, using bw model

Run on: June 6, 2006, 04:47:35 ; Search time 8.14053 Seconds
(Without alignments) 1607.447 Million cell updates/sec

Title: US-10-724-274-20
Perfect score: 722
Sequence: 1 NAVLGILCLVTPSPCVLSQ.....HGTYYGMTTGDA LDYNGQG 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing First 45 summaries

Database : PIR 80:*

1: Pirl1:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	584	80.9	144	2 S11244	Ig gamma-2a chain
2	550	76.5	144	1 G2MS14	Ig heavy chain pre
3	539	74.7	141	2 S52446	Ig heavy chain V r
4	535	74.2	140	2 S50328	Ig heavy chain V r
5	533	73.8	135	2 S31913	Ig gamma-2A chain
6	523	72.4	117	2 S10111	Ig heavy chain V r
7	520	72.0	139	2 A32456	Ig heavy chain pre
8	519	71.9	115	1 HVM514	Ig heavy chain pre
9	499	69.5	140	2 S14228	Ig gamma-1 chain P
10	497	68.8	116	1 GIM510	Ig mu chain precur
11	496	68.7	116	2 A33932	Ig heavy chain V r
12	477	66.1	101	2 S03466	Ig heavy chain V r
13	473	65.5	117	2 S38563	Ig heavy chain V r
14	473	65.5	122	2 S20809	Ig heavy chain V r
15	465	64.4	122	2 A49049	Ig heavy chain V r
16	460	63.7	120	2 PL0087	Ig heavy chain V r
17	458	63.5	112	2 S11100	Ig heavy chain V r
18	454	63.0	106	2 S14489	Ig heavy chain V r
19	454	63.0	114	2 S11096	Ig heavy chain V r
20	452	62.7	114	2 S11099	Ig heavy chain V r
21	448	62.1	116	2 S11102	Ig heavy chain V r
22	446	61.8	113	2 S11101	Ig heavy chain V r
23	445	61.7	111	2 S26324	Ig heavy chain V r
24	445	61.5	118	2 P00266	Ig heavy chain V r
25	445	61.5	121	2 P4155	Ig gamma-2b chain
26	445	61.6	116	2 S42484	Ig heavy chain V r
27	444	61.5	107	2 S14492	Ig heavy chain V r
28	443	61.4	112	2 S11108	Ig heavy chain V r
29	443	61.4	118	2 S32786	Ig heavy chain (an

ALIGNMENTS

RESULT 1	Score	DB ID	Description
S11244	584	DBP 60	Ig gamma-2a chain precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)			
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996			
C;Accession: S11244			
R;Wellman, A.A.; Meares, C.F. 1990			
Nucleic Acids Res. 18, 5201.			
A;Title: Sequences of the Lym-1 antibody heavy and light chain variable regions.			
A;Reference number: S11244; MUID:90384832; PMID:2119497			
A;Accession: S11244			
A;Molecule type: mRNA			
A;Residues: 1-144 <WEL>			
C;Cross-references: UNIPARC:UPI0000176CB1; EMBL:X53483			
C;Super-organisms: immunoglobulin V region; immunoglobulin homology			
P;34-116/Domain: immunoglobulin homology <IMM>			
Query Match 80.9t; Score 584; DB 2; Length 144;			
Best Local Similarity 84.6t; Pred. No. 3.e-44;			
Matches 115; Conservative 5; Mismatches 10; Indels 6; Gaps 2;			
QY 1 MAVLGILCLVTPSPCVLSQVQLRESGGPLVADPSQSLTDTGYHWRQDP 60			
Db 1 MAVLGILCLVTPSPCVLSQVQLKESGPLVADPSQSLTDTGYHWRQDP 60			
QY 61 GKCLEWLYVWVSPGDSYSTNSALKSRSRMTIKRDKNSKSYVPLIMNSLQTDSSAMYCARHGTY 120			
Db 61 GKCLEWLYVWVSPGDSYSTNSALKSRSRMTIKRDKNSKSYVPLIMNSLQTDSSAMYCARHGTY 120			
QY 121 YGMMTTGDA LDYNGQG 136			
Db 118 YGSPYL--AFASNGHG 130			

RESULT 2

Q2H514	Score	DB ID	Description
Q;Species: Mus musculus (house mouse)			
C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 09-Jul-2004			
C;Accession: A02054			
R;Sakano, H.; Maki, R.; Roeder, W.; Tonegawa, S.			
Nature 286, 676-683, 1980			
A;Title: Two types of somatic recombination are necessary for the generation of complete immunoglobulin genes.			
A;Reference number: A93229; MUID:81012133; PMID:6774258			
A;Accession: A02054			
A;Molecule type: DNA			
A;Residues: 1-144 <SAK>			
C;Cross-references: UNIPROT:P01819; UNIPARC:UPI000002726A; GB:U00491; GB:J00491;			
C;Note: the sequence shown was determined from a differentiated gene isolated from a m;			
A;Note: the authors translated the codon TAT for residue 51 as Thr and TTA for residue 51.			
C;Genetics:			

Scoring table:	BLOSUM62	ALIGMENTS				
Gapop:	10.0					
Searched:	2849598 seqs, 925015592 residues					
Total number of hits satisfying chosen parameters:	2849598					
Minimum DB seq length:	0					
Maximum DB seq length:	200000000					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
Database :	UniProt_7.2: 1: uniprot_sprot: 2: uniprot_trembl: *					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Score	Query	Match	Length	DB ID	Description
1	573	79.4	484	2	Q5U472_MOUSE	Q5u472 mus musculu
2	550	76.2	144	1	R943_MOUSE	R91x92 mus musculu
3	538	74.5	482	2	Q51Q19_RAT	Q91x92 rattus norv
4	528	73.1	591	2	Q51Q19_RAT	Q91x92 rattus norv
5	517.5	71.9	115	1	HV44_MOUSE	P01820 mus musculu
6	517.5	71.9	469	2	Q5W839_RAT	Q86839 rattus norv
7	509.5	70.6	477	2	Q51Q11_RAT	Q51Q11 rattus norv
8	501.9	69.5	458	2	Q5MB42_RAT	Q5MB42 rattus norv
9	497	68.8	116	1	HV45_MOUSE	P01821 mus musculu
10	451	62.5	121	2	Q99NQ4_MOUSE	Q99NQ4 mus musculu
11	373.5	52.1	135	1	P20957_XENLA	P20957 xenopus lae
12	373.5	51.7	560	2	Q4V801_XENLA	Q4V801 xenopus lae
13	370	51.2	485	2	Q561M5_MOUSE	Q561M5 mus musculu
14	359.13	51.2	483	2	Q5U113_MOUSE	Q54113 mus musculu
15	367.5	50.9	487	2	Q58R33_MOUSE	Q58R33 mus musculu
16	366.5	50.5	485	2	Q58S54_MOUSE	Q58S54 mus musculu
17	360.5	49.9	476	2	Q6GRX1_HUMAN	Q6GRX1 homo sapien
18	359	49.7	617	2	Q569B3_RAT	Q569b3 rattus norv
19	357	49.4	615	2	Q569B6_RAT	Q569b6 rattus norv
20	355	49.2	477	2	Q6GRX7_HUMAN	Q6GRX7 homo sapien
21	353	48.9	465	2	Q6GRX6_HUMAN	Q6GRX6 homo sapien
22	351.5	48.7	136	1	HV01_XENLA	P2956 xenopus lae
23	352	48.5	136	1	Q6LBQ5_MOUSE	Q6LBQ5 mus musculu
24	348	48.2	496	2	Q5VUR6_RAT	Q5VUR6_rattus norv
25	345	47.8	482	2	Q5VUR7_HUMAN	Q5VUR7 homo sapien
26	344	47.7	573	2	Q8W038_HUMAN	Q8W038 homo sapien
27	344	47.6	620	2	Q963Y0_HUMAN	Q963Y0_HUMAN
28	342.5	47.6	493	2	Q569J1_HUMAN	Q569J1 homo sapien
29	342	47.4	137	1	HV46_MOUSE	P01822 mus musculu
30	341	47.2	576	2	Q6PA18_HUMAN	Q6PA18 homo sapien
31	340.5	47.2	595	2	Q3BBR4_RAT	Q3BBR4 rattus norv

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OM protein - protein search, using BW model

Run on: June 6, 2006, 04:59:30 ; Search time 47.5355 Seconds
(without alignments)

830.460 Million cell updates/sec

Title: US-10-724-274-25

Perfect score: 2400

Sequence: 1 QVQLKESGPGLVAPSSLSI.....MHEALHNHYTOKSLSISSLGK 451

Scoring table: BLOSUM62

Gapop: 10.0 , Gapext: 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Issued Patents_AA:*

1: /BMC_Celerra_SIDS3/podata/2/iaas/5_COMB.pep:*

2: /BMC_Celerra_SIDS3/podata/2/iaas/6_COMB.pep:*

3: /BMC_Celerra_SIDS3/podata/2/iaas/7_COMB.pep:*

4: /BMC_Celerra_SIDS3/podata/2/iaas/H_COMB.pep:*

5: /BMC_Celerra_SIDS3/podata/2/iaas/PCTUS_COMB.pep:*

6: /BMC_Celerra_SIDS3/podata/2/iaas/RE_COMB.pep:*

7: /BMC_Celerra_SIDS3/podata/2/iaas/backfile1.pep:*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2072	86.3	443	5 PCT-US96-13152-4	Sequence 4, Appli
2	2063.5	86.0	467	1 US-08-704-744-81	Sequence 81, Appli
3	2057	85.7	460	2 US-10-630-406-5	Sequence 5, Appli
4	2033.5	84.7	467	2 US-08-523-594-8	Sequence 8, Appli
5	2026.5	84.4	467	2 US-08-523-894-10	Sequence 10, Appli
6	2021.5	84.2	467	2 US-08-523-894-12	Sequence 12, Appli
7	2020.5	84.2	446	2 US-08-397-111-7	Sequence 7, Appli
8	2011.5	83.8	467	1 US-07-216-098A-45	Sequence 45, Appli
9	1981	82.5	464	2 US-09-472-087-2	Sequence 2, Appli
10	1981	82.5	464	2 US-09-472-087-66	Sequence 66, Appli
11	1977	82.4	451	2 US-09-472-087-70	Sequence 70, Appli
12	1976.5	82.4	463	2 US-09-472-087-74	Sequence 4, Appli
13	1976.5	82.4	463	2 US-09-472-087-68	Sequence 68, Appli
14	1970.5	82.1	463	2 US-09-472-087-1	Sequence 63, Appli
15	1970.5	82.1	463	2 US-09-472-087-63	Sequence 64, Appli
16	1964.5	81.9	463	2 US-09-472-087-64	Sequence 41, Appli
17	1961.5	81.3	467	2 US-08-030-175-41	Sequence 4, Appli
18	1959.5	81.2	473	2 US-09-039-672A-4	Sequence 222, Appli
19	1947.5	81.1	450	2 US-09-996-288-222	Sequence 224, Appli
20	1947.5	81.1	450	2 US-09-996-288-224	Sequence 222, Appli
21	1947.5	81.1	450	2 US-09-996-265-222	Sequence 224, Appli
22	1947.5	81.1	450	2 US-09-996-265-224	Sequence 224, Appli
23	1947.5	81.1	467	2 US-08-030-175-42	Sequence 210, Appli
24	1945.5	81.1	450	2 US-09-996-288-210	Sequence 220, Appli
25	1945.5	81.1	450	2 US-09-996-288-220	Sequence 220, Appli
26	1945.5	81.1	450	2 US-09-996-288-238	Sequence 238, Appli

ALIGNMENTS

RESULT 1
PCT-US96-13152-4
Sequence 4, Application PC/TUS9613152
GENERAL INFORMATION:
APPLICANT: Martin, Ulrich, et al.
TITLE: Anti-Selectin antibodies for prevention of multiple organ failure
CORRESPONDENCE ADDRESS:
ADDRESSEE: Attn: Norman D. Hanson
FELLE & Lynch
STREET: 805 Third Avenue
CITY: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PPP/NDH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-2200
TELEFAX: (212) 638-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13152-4

Copyright (c) 1993 - 2006 Biocceleration Ltd.
 OM protein - protein search, using sw model.
 Run on: June 6, 2006, 04:47:35 ; search time 26.9954 seconds
 (without alignments) 1607.447 Million cell updates/sec

Title: US-10-724-274-25
 Perfect score: 2400
 Sequence: 1 QVQLKESGPGLVAPPQQLS1.....MHEALHNHYTQKSLSLIGK 451

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum March 01
 Maximum March 100%
 Listing first 45 summaries

Database : PIR-80.* ;
 1: PIR1:/*
 2: PIR2:/*
 3: PIR3:/*
 4: PIR4:/*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1743	72.6	327	1	G4HU		Ig gamma-4 chain C
2	1605.5	65.9	326	1	G2HU		Ig gamma-2 chain C
3	1590.5	66.3	330	1	GHHU		Ig gamma-1 chain C
4	1585	66.0	377	2	A60764		Ig gamma-3 chain C
5	1575	65.6	377	2	A23511		Ig gamma-3 chain C
6	1554	64.8	470	2	S22080		Ig heavy chain pre
7	1519	62.3	472	2	S31459		Ig gamma-1 chain pre
8	1423.5	59.3	444	2	PC4436		monoclonal antibody
9	1417	59.0	446	2	S40295		Ig gamma-2a chain
10	1412.5	58.9	469	2	S37483		Ig gamma-2a chain
11	1411	58.8	374	2	S69339		Ig heavy chain V _r
12	1305	54.4	474	1	G2MS11		Ig gamma-2b chain
13	1289.5	53.7	328	2	I47159		Ig gamma-2a chain
14	1289.5	53.7	475	2	S01321		Ig gamma-2b chain
15	1283.5	53.5	328	2	I47160		Ig gamma-2b chain
16	1264.5	52.7	328	2	I47161		Ig gamma-3 chain C
17	1240.5	51.7	328	2	I47158		Ig gamma-1 chain C
18	1199	50.0	323	1	GHRB		Ig gamma-1 chain C
19	1162	48.4	329	1	C2GP		Ig gamma-2 chain C
20	1147	47.8	308	2	C30554		Ig heavy chain C _r
21	1139.5	47.5	255	4	S31866		Ig gamma-1 chain C _r
22	1129	47.1	234	2	PT0207		Ig gamma-1 chain C _r
23	1124	46.8	333	2	PS0018		Ig gamma-2b chain
24	1118.5	46.6	326	2	PS0017		Ig gamma-1 chain C _r
25	1108	46.2	289	1	G3HUWI		Ig gamma-3 heavy C
26	1108	46.2	329	1	S00847		Ig gamma-2c chain
27	1106.5	46.1	324	1	G1MSA		Ig gamma-1 chain C
28	1106.5	46.1	330	2	S06611		Ig gamma-2 chain C
29	1103	46.0	327	2			

RESULT 1

G4HU

Ig gamma-4 chain C region - human

C;Species: Homo sapiens (man)
 C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004

C;Accession: A90313; A90249; A02150
 R;Ellison, J. ; Buxbaum, J. ; Hood, L.

DNA 1, 11-18, 1981
 A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A;Reference number: A90933; MUID:83157104; PMID:6299662

A;Accession: A90933

A;Molecule type: DNA

A;Residues: 1-327 <ELL>

A;Cross-references: UNIPARC:UPI000047190

A;Note: the sequence was determined from the germline gene
 R;Pink, J.R.L. ; Buttery, S.H. ; De Vries, G.M. ; Milstein, C.

Biochem. J. 117, 33-47, 1970
 A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A;Reference number: A90249; MUID:70207560; PMID:4192699

A;Accession: A90249

A;Molecule type: protein

A;Residues: 1-30,81-326 <PIN>

A;Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796

C;General: C

A;Gene: GDB:1IGHG4

A;Cross-references: GDB:119240; OMIM:147130

A;Map position: 1q032.33-1q432.33

A;Introns: 99/1, 111/1, 221/1
 C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (κ) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a superfamily: immunoglobulin C region, immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin homology <IM1>

F;20-85/Domain: immunoglobulin homology <IM1>

F;99-110/Region: hinge

F;134-205/Domain: immunoglobulin homology <IM2>

F;14/Disulfide bonds: interchain (to light chain) #status predicted

F;27,83,141-201,241-305/Disulfide bonds: interchain (to heavy chain) #status experimental

F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;117/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 1743; DB 1; Length 327;

Best Local Similarity 100.0%; Pred. No. 5 5e-95;
 Matches 327; Conserv. 0; Mismatches 0; Gaps 0;

QY 125 ASTKGPSVPLAPCPSRSTSSTAGCLVDRYPPRPVTVSNSGALTSGVHTFPVQVLOSS 184
 1 ASTKGPSVPLAPCPSRSTSSTAGCLVDRYPPRPVTVSNSGALTSGVHTFPVQVLOSS 60
 DB 61 GLYSLSVVTVPSSSLGKTYTCTNDHCPNTKTDKPSNTKTDHCPNTKTDHCPNTKTDHCPNTK 244
 61 GLYSLSVVTVPSSSLGKTYTCTNDHCPNTKTDKPSNTKTDHCPNTKTDHCPNTKTDHCPNTK 120

ALIGNMENTS

Copyright (c) 1993 - 2006 Biocceleration Ltd.
 Gendcore version 5.1.9
 OM protein - protein search, using sw mode!
 Run on: June 6, 2006, 04:37:25 ; Search time 208.628 Seconds
 Title: US-10-724-274-25
 Perfect score: 24.00
 Sequence: 1 QVQLKESGPGLVAPSQSLSI.....MHEALHNHYTQKSLSLSLGK 451

Scoring table: BLOSUM62 Gapext 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*;

Maximum Match 10*;

Listing first 45 summaries

Database : UniProt_7.2.*
 1: uniprot_sprot:
 2: uniprot_trembl:
 *

Prd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2041.5	85.1	476	2	Q6M2X7_HUMAN		
2	2014	83.9	473	2	Q8TC63_HUMAN		
3	1948	81.2	476	2	Q6GMX1_HUMAN		
4	1943	81.2	472	2	Q6N089_HUMAN		
5	1939.5	80.8	465	2	Q5GMX6_HUMAN		
6	1939	80.8	469	2	Q569P4_HUMAN		
7	1918	79.9	478	2	Q8P181_HUMAN		
8	1916	79.8	470	2	Q8PJA4_HUMAN		
9	1914	79.8	465	2	Q6P6C4_HUMAN		
10	1912	79.7	464	2	Q6M2U6_HUMAN		
11	1905	79.4	466	2	Q6IN78_HUMAN		
12	1902	79.2	470	2	Q725W1_HUMAN		
13	1900.5	79.2	475	2	Q5BFB5_HUMAN		
14	1898	79.0	544	2	Q6P9J5_HUMAN		
15	1894	78.9	470	2	Q8CNA4_HUMAN		
16	1891.5	78.8	473	2	Q6M2V7_HUMAN		
17	1886	78.8	482	2	Q72351_HUMAN		
18	1882.5	78.6	480	2	Q6N094_HUMAN		
19	1882.5	78.4	475	2	Q6GMW7_HUMAN		
20	1877.5	78.2	481	2	Q6N097_HUMAN		
21	1877.5	78.2	466	2	Q6N096_HUMAN		
22	1870.5	77.9	475	2	Q6M2Q6_HUMAN		
23	1869.5	77.9	475	2	Q6N095_HUMAN		
24	1866.5	77.8	473	2	Q6P055_HUMAN		
25	1855.5	77.4	521	2	Q8NAY9_HUMAN		
26	1851.5	77.1	519	2	Q5BEM2_HUMAN		
27	1848	77.0	417	2	Q6N093_HUMAN		
28	1838	76.6	518	2	Q6N030_HUMAN		
29	1829	76.2	480	2	Q6P0F1_HUMAN		
30	1821.5	75.9	469	2	Q727P5_HUMAN		
31	1820.5	75.9	475	2	Q5RBE17_PONY		

ALIGNMENTS

RESULT 1	Q6M2X7_HUMAN	PRELIMINARY;	PRT;	476 AA.
ID	Q6M2X7_HUMAN			
AC	Q6M2X7;			
DT	05-JUL-2004	Integrated into UniProtKB/TREMBL.		
DT	05-JUL-2004	Sequence version 13.		
DT	07-FEB-2006	entry version 13.		
DB	Hypothetical protein DK2ZP68M24218.			
GN	Name=DK2ZP68M24218;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo;			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Human rectum tumor;			
RG	The German Human cDNA Consortium;			
RA	Bloecher H., Boecker M., Mewes H.W., Weil B., Amid C., Obanger A.,			
RA	Fobo G., Han M., Wiemann S.;			
RL	Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.			
CC				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NonDerivs License			
DR	EMBL; BX640824; CAB45900.1; -; mRNA.			
DR	HSSP; P01861; 1AQD.			
DR	SMR; Q6M2X7; 28-472.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_c1.			
DR	InterPro; IPR030597; Ig_RHC.			
DR	InterPro; IPR033596; Ig_v.			
DR	InterPro; IPR013106; V-Set.			
DR	PFam; PF01654; C1-set; 3.			
DR	SMART; SM00409; Ig; 1.			
DR	SMART; SM00407; IgCl-1.			
DR	SMART; SM00406; IgV; 1.			
DR	PROSITE; PS50835; Ig_LIKE; 4.			
DR	PROSITE; PS00230; Ig_MHC; UNKNOWN_2.			
KW	Hypothetical protein.			
SQ	SEQUENCE 476 AA;			
Query Match	85.1*	Score 2041.5;	DB 2;	Length 476;
Best Local Similarity	85.0*	Pred. No. 4.1-135;	Indels 5;	Gaps 2;
Matches 385;	Conservative 25;	Mismatches 38;		
QY	1 QVQLKESGPGLVAPSQSLSI.....MHEALHNHYTQKSLSLSLGK 451			
Db	27 QIQLQESGPGLVUKSAETLSLICSPDGLVSSSSWVIRQPGQLEWIGTVSYSTPY 86			
QY	59 YNSALKSRSRMTIRKDNKSQSQVFLIMMSNQTDPSAMMYCARHGTYGMMTTGDAIDWGGT 118			
Db	87 YTPSLKSRSLTHVDPSSKQIPNLNTSVAUTAVYCVRHG--GYSFASAYPPNGQGA 143			

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OM protein - protein search, using bw mode].

Run on: June 6, 2006, 04:37:11 ; Search time 88.4528 seconds
(without alignments) 88.4528 seconds
Perfect score: 1225
Sequence: 1 QVQLKESGPQLVAPQSLSI.....PSNTKVDKRVESKYGPPCPS 232

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0#
Maximum Match 100#
Listing first 45 summaries

Database : A_Geneseq_ip8:
1: geneseq_ip1980s:
2: geneseq_ip1990s:
3: geneseq_ip2000s:
4: geneseq_ip2001s:
5: geneseq_ip2002s:
6: geneseq_ip2003as:
7: geneseq_ip2003bs:
8: geneseq_ip2004s:
9: geneseq_ip2005s:
10: geneseq_ip2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	100.0	232	8 ADQ31887	Adq31887 Antibody
2	1225	100.0	232	8 ADT77646	Adt77646 Antibody
3	1225	100.0	232	9 ABB51165	Aeb51165 Chimeric
4	1225	100.0	451	8 ADQ31884	Adq31884 Antibody
5	1225	100.0	451	8 ADT51712	Adt51712 M200 anti
6	1225	100.0	451	8 ADT51711	Adt51711 M200 anti
7	1225	100.0	451	8 ADT51709	Adt51709 M200 anti
8	1225	100.0	451	8 ADT51713	Adt51713 M200 anti
9	1225	100.0	451	8 ADT51710	Adt51710 M200 anti
10	1225	100.0	451	8 ADT77643	Adt77643 Antibody
11	1225	100.0	451	9 ABB51162	Aeb51162 Chimeric
12	1225	100.0	451	10 AEF12090	Aef12090 Anti-alpha
13	1225	100.0	451	10 AEF16428	Aef16428 Chimeric
14	1225	100.0	451	10 AEF16425	Aef16425 Chimeric
15	1225	100.0	451	10 AEF16426	Aef16426 Chimeric
16	1225	100.0	451	10 AEF16427	Aef16427 Chimeric
17	1225	100.0	451	10 AEF16424	Aef16424 Chimeric
18	1107	90.4	451	8 ADQ31890	Adq31890 Antibody
19	1107	90.4	451	9 AEF51168	Aef51168 Chimeric
20	997	81.4	462	8 ADF77154	Adf77154 Chimeric
21	996.5	80.9	442	9 ADY74779	Rat anti-
22	987.5	80.1	476	4 AAB49243	Aab49243 Chimeric
23	978.5	79.9	468	5 AAE27928	Human C5B

ALIGNMENTS

RESULT 1
ADQ31887
ID ADQ31887 standard; protein; 232 AA.
XX ADQ31887;
XX DT 23-SEBP-2004 (first entry)
XX DE Antibody F200 heavy chain amino acid sequence SEQ ID NO:28.
XX KW chimeric anti-alpha5beta1 integrin antibody; antibody; immunoreactive;
KW chimeric anti-alpha5beta1 integrin antibody; humanised anti-alpha5beta1 integrin antibody;
KW vascularization; antiangiogenesis; integrin alpha5beta1 antagonist.
XX KW Mus sp.
OS Homo Sapiens.
OS Synthetic.
XX PN WO2004056308-A2.
XX PD 08-JUL-2004.
XX PP 26-NOV-2003; 2003WO-US038172.
XX PR 26-NOV-2003; 2003WO-US038172.
XX XX
XX XX
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX XX
XX PI Ramakrishnan V, Powers D, Johnson DE, Jeffry U,
XX PT
XX DR 2004-525316/50.
XX DR N-PSDB; ADQ31886.
XX XX
XX PT New chimeric anti-alpha-5 beta-1 integrin antibody useful for controlling
PT vascularization in injured tissue.
XX XX
XX PS Claim 23; SEQ ID NO 28; 89pp; English.

The present invention describes a chimeric anti-alpha5beta1 integrin antibody (1), comprising: (a) a first polypeptide sequence from a first source comprising one or more amino acid sequences selected from SEQ ID NO: 1, 7, 16, 18, 20, 22, 25, 26, 28, 31 and 32; and (b) a second polypeptide from a second source comprising a constant region sequence of an antibody of the second source, where the first and second polypeptide sequences form a protein complex that is immunoreactive with alpha5beta1 integrin. Also described: (1) purifying (M1) pH-sensitive (1) comprises

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OM protein - protein search, using BW model.

Run on: June 6, 2006, 04:47:35 ; search time 13.8868 seconds
1607.447 Million cell updates/sec

Title: US-10-724-274-28
Perfect score: 1225
Sequence: 1 QVQRIKESGPGLVAP-QSLSI.....PSNTKVDKRVBSKY/GPPCP5 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80;*
1: pi1;*
2: pi2;*
3: pi3;*
4: pi4;*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	789	64.4	231	2	PC4155	Ig gamma-2b chain
2	785.5	64.1	220	2	A49444	Ig gamma-1 heavy C
3	750.5	61.3	241	2	S69131	Ig heavy chain (PO
4	721	58.9	470	2	S22080	Ig heavy chain pre
5	694	56.7	472	2	S31459	Ig gamma-1 chain -
6	660	53.9	246	2	S38950	Ig gamma chain - m
7	660	53.9	446	2	S40295	Ig gamma-2a chain
8	640.5	52.3	469	2	S37483	Ig gamma-2a chain
9	631.5	51.6	444	2	PC4436	monoclonal antibody
10	626.5	51.1	220	2	S68211	Ig heavy chain (Ma
11	620.5	50.7	548	2	S38864	Ig epsilon chain C
12	611	49.9	213	2	S68213	Ig heavy chain (Ma
13	578.5	47.2	475	2	S01321	Ig gamma-2b chain
14	577	47.1	221	2	S49220	Ig gamma-1 chain -
15	573.5	47.0	214	2	PC4202	monoclonal antibody
16	573.5	46.8	254	2	B31790	Ig heavy chain V r
17	568	46.4	327	1	G4HU	Ig gamm-4 chain C
18	567	46.3	474	1	G2MS11	Ig gamma-2b chain
19	552	45.1	549	2	S04845	Ig heavy chain pre
20	529	43.2	144	2	S11244	Ig gamma-2 chain C
21	513.5	41.9	326	1	G2HU	Ig gamma-1 chain P
22	508.5	41.5	140	2	S14238	Ig heavy chain V r
23	503	41.1	122	2	S20809	Ig gamma-3 chain C
24	501	40.9	377	2	A23511	Ig gamma-3 chain C
25	501	40.9	377	2	A60764	Ig heavy chain pre
26	500.5	40.9	144	1	G2MS14	Ig heavy chain V r
27	499	40.7	117	2	S38563	Ig heavy chain V r
28	498	40.7	122	2	A49049	Ig mu chain - shee
29	496	40.5	592	2	S25705	

ALIGNMENTS

RESULT 1	Query	Match	Score	DB	Length	231;
PC4155	IG Gamm-2b chain V-C region Mabb23 - mouse	PC4155	64.4%	PC4155	64.4%	Score: 789; Pred: No. 1. 98-47; Missmatches 26; Indels 41; Gaps 4;
	C:Species: Mus musculus (house mouse)					Matches 157; Conservative 1:1; Note: This protein has unusual amino acid compared with the conserved sequences of mabb23.
	C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000					C:Accession: PC4155
	C:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a new immunoglobulin homology protein. Unique D sequence F:03-119/Region: V region F:119-203/Domain: immunoglobulin homology <IMM>					
	A:Residues: 1-231 <KWA>					A;Accession: PC4155
	A:Cross-References: UNIPARC:UPI00001157CB; GB:U28970; PID:91262180; PID: AAC52489.1; P:R;I;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.					A;Note: C:Superfamily: immunoglobulin C region; immunoglobulin homology P:1-231/Product: unique D sequence F:03-119/Region: V region F:119-203/Domain: immunoglobulin homology <IMM>

Search Results for Query: PIR80:*						
Database: BLOSUM62						
Searcher: BLOSUM62						
Search date: June 6, 2006, 04:47:35 ; Search time: 26.9954 Seconds (without alignments)						
DB length: 1607.447	Million cell updates/sec					
DB seq length: 2399						
DB score: 1	EVQLVVEGGGLVQPGGSLRL.....MHEALHNHYTQKSLSLIGK 451					
Ring table: BLOSUM62						
Gap open: 10.0 , Gapext: 0.5						
Number of hits satisfying chosen parameters: 283416						
al number of hits satisfying chosen parameters:						
Minimum DB seq length: 0						
Maximum DB seq length: 2000000000						
Bit-processing: Minimum Match 0% Maximum Match 100%						
Listing First 45 Summaries						
1: PIR80:*						
2: pir1:*						
3: pir2:*						
4: pir3:*						
4: pir4:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Filt. No.	Score	Query Match	Length	DB ID	Description	
1	1743	72.7	327	G4HU	Ig gamma-4 chain C	
2	1605.5	66.9	326	G2HU	Ig gamma-2 chain C	
3	1590.5	66.3	330	GHHU	Ig gamma-1 chain C	
4	1585	66.1	377	A60764	Ig gamma-3 chain C	
5	1575	65.7	377	A23511	Ig gamma-3 chain C	
6	1524	63.5	470	S22080	Ig gamma-2a chain C	
7	1479	61.7	472	S31459	Ig gamma-1 chain pre-mooclonal antibody	
8	1466.5	61.1	444	PC4436	Ig gamma-2a chain	
9	1436.5	59.9	469	S37483	Ig gamma-2a chain	
10	1431	59.6	446	S40295	Ig gamma-2a chain	
11	1373	57.2	374	S69339	Ig heavy chain V _r	
12	1344	56.0	474	G2MS11	Ig gamma-2b chain	
13	1324	55.2	475	S01321	Ig gamma-2b chain	
14	1289.5	53.8	328	I47159	Ig gamma-2a chain	
15	1283.5	53.5	328	I47160	Ig gamma-2b chain	
16	1264.5	52.7	328	I47161	Ig gamma-3 chain C	
17	1240.5	51.7	328	I47158	Ig gamma-1 chain C	
18	1199	50.0	323	GHRB	Ig gamma chain C	
19	1162	48.4	308	C3GPP	Ig gamma-2 chain C	
20	1147	47.8	329	C30554	Ig heavy chain C	
21	1139.5	47.5	255	S31866	Ig gamma-1 chain C	
22	1129.5	47.1	234	PT0207	Ig gamma chain C	
23	1124	46.9	333	PS0018	Ig gamma-2b chain	
24	1118.5	46.6	326	PS0017	Ig gamma-1 chain C	
25	1108.5	46.2	329	G3RUWI	Ig gamma-3 heavy C	
26	1108	46.2	308	S00847	Ig gamma-2c chain	
27	1106.5	46.1	324	G1MS	Ig gamma-1 chain C	
28	1105	46.0	330	S00631	Ig gamma-2 chain C	
29	1103	46.0	327	S00511	Ig gamma-3 chain C	
30	1101.5	45.9	393	1	Ig gamma-1 chain C	
31	1101.5	45.9	399	1	Ig gamma-2a chain	
32	1099	45.8	335	1	Ig gamma-2a chain	
33	1098.5	45.8	329	1	Ig gamma-3 chain C	
34	1090.5	45.5	398	1	Ig gamma-4 chain C	
35	1090.5	45.2	277	2	I47162	
36	1084.5	45.2	322	2	PS0019	
37	1049.5	43.7	405	1	G2MSBM	
38	1025	42.7	548	2	S38864	
39	891.5	37.2	549	2	S04845	
40	835.5	34.8	241	2	S69131	
41	831.5	34.7	249	2	S69340	
42	821.5	34.2	572	2	B46529	
43	766	31.9	218	2	A36040	
44	756.5	31.5	220	2	A49444	
45	754	31.4	246	2	S38950	

